

SEQUENCE LISTING

<110> Ingraham, Holly A.
Krylova, Irina

<120> Steroidogenic Factor-1 Protein Variants
and Methods of Making Same

<130> 66778-120

<150> US 60/395,371

<151> 2002-07-12

<160> 33

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<212> PRT

<213> Mus musculus

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Pro	Tyr	Ser	Tyr	Pro	Glu	Pro	Phe	Ser	Gly	Gly	Pro	Asn	Val	Pro	Glu
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Ala	Arg	Ile	Val	Gly	Cys	Leu	Gln	Glu	Pro	Ala	Lys	Ser	Arg	Ser	Asp
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Gln	Pro	Ala	Pro	Phe	Ser	Leu	Leu	Cys	Arg	Met	Ala	Asp	Gln	Thr	Phe
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Ile	Ser	Ile	Val	Asp	Trp	Ala	Arg	Arg	Cys	Met	Val	Phe	Lys	Glu	Leu
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Glu	Val	Ala	Asp	Gln	Met	Thr	Leu	Leu	Gln	Asn	Cys	Trp	Ser	Glu	Leu
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Leu	Val	Leu	Asp	His	Ile	Tyr	Arg	Gln	Val	Gln	Tyr	Gly	Lys	Glu	Asp
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Ser	Ile	Leu	Leu	Val	Ser	Gly	Gln	Glu	Val	Glu	Leu	Ser	Thr	Val	Ala
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Val	Gln	Ala	Gly	Gly	Leu	Leu	His	Ser	Leu	Val	Leu	Arg	Ala	Gln	Glu
				165					170					175	
Leu	Val	Leu	Gln	Leu	His	Ala	Leu	Gln	Leu	Asp	Arg	Gln	Glu	Phe	Val
			180					185					190		
Cys	Leu	Lys	Phe	Leu	Ile	Leu	Phe	Ser	Leu	Asp	Val	Lys	Phe	Ile	Asn
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Asn	His	Ser	Leu	Val	Lys	Asp	Ala	Gln	Glu	Lys	Ala	Asn	Ala	Ala	Leu
	210					215						220			

Leu	Asp	Tyr	Thr	Leu	Cys	His	Tyr	Pro	His	Cys	Gly	Asp	Lys	Phe	Gln
225					230					235					240
Gln	Leu	Leu	Cys	Leu	Val	Glu	Val	Arg	Ala	Leu	Ser	Met	Gln	Ala	Lys
			245						250					255	
Glu	Tyr	Leu	Tyr	His	Lys	His	Leu	Gly	Asn	Glu	Met	Pro	Arg	Asn	Asn
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Leu	Leu	Ile	Glu	Met	Leu	Gln	Ala	Lys	Gln	Thr					
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<211> 288

<212> PRT

<213> Homo sapiens

<400> 2

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			20					25					30		
Tyr	Gly	Tyr	Pro	Glu	Pro	Phe	Ser	Gly	Gly	Pro	Asn	Val	Pro	Glu	Leu
		35					40					45			
Ile	Leu	Gln	Leu	Leu	Gln	Leu	Glu	Pro	Asp	Glu	Asp	Gln	Val	Arg	Ala
	50				55					60					
Arg	Ile	Leu	Gly	Cys	Leu	Gln	Glu	Pro	Thr	Lys	Ser	Arg	Pro	Asp	Gln
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Pro	Ala	Ala	Phe	Gly	Leu	Leu	Cys	Arg	Met	Ala	Asp	Gln	Thr	Phe	Ile
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Ser	Ile	Val	Asp	Trp	Ala	Arg	Arg	Cys	Met	Val	Phe	Lys	Glu	Leu	Glu
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Val	Ala	Asp	Gln	Met	Thr	Leu	Leu	Gln	Asn	Cys	Trp	Ser	Glu	Leu	Leu
		115					120					125			
Val	Phe	Asp	His	Ile	Tyr	Arg	Gln	Val	Gln	His	Gly	Lys	Glu	Gly	Ser
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Ile	Leu	Leu	Val	Thr	Gly	Gln	Glu	Val	Glu	Leu	Thr	Thr	Val	Ala	Thr
145					150					155					160
Gln	Ala	Gly	Ser	Leu	Leu	His	Ser	Leu	Val	Leu	Arg	Ala	Gln	Glu	Leu
			165						170					175	
Val	Leu	Gln	Leu	Leu	Ala	Leu	Gln	Leu	Asp	Arg	Gln	Glu	Phe	Val	Cys
			180					185					190		
Leu	Lys	Phe	Val	Cys	Leu	Lys	Phe	Ile	Ile	Leu	Phe	Ser	Leu	Asp	Leu
		195					200					205			
Lys	Phe	Ile	Asn	Asn	His	Ile	Leu	Val	Lys	Asp	Ala	Gln	Glu	Lys	Ala
	210					215					220				
Asn	Ala	Ala	Leu	Leu	Asp	Tyr	Thr	Leu	Cys	His	Tyr	Pro	His	Cys	Gly
225					230					235					240
Asp	Lys	Phe	Gln	Gln	Leu	Leu	Leu	Cys	Leu	Val	Glu	Val	Arg	Ala	Leu
			245						250					255	
Ser	Met	Gln	Ala	Lys	Glu	Tyr	Leu	Tyr	His	Lys	His	Leu	Gly	Asn	Glu
			260					265					270		
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<212> PRT
<213> Mus musculus

<400> 3
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Lys Ser Glu Tyr Pro Asp Pro Tyr Ser Ser Ser Pro Glu Ser Met Met
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35 40 45
Pro Leu Leu Ile Leu Glu Leu Leu Lys Cys Glu Pro Asp Glu Pro Gln
50 55 60
Val Gln Ala Lys Ile Met Ala Tyr Leu Gln Gln Glu Gln Ser Asn Arg
65 70 75 80
Asn Arg Gln Glu Lys Leu Ser Ala Phe Gly Leu Leu Cys Arg Met Ala
85 90 95
Asp Gln Thr Leu Phe Ser Ile Val Glu Trp Ala Arg Ser Ser Ile Phe
100 105 110
Phe Arg Glu Leu Lys Val Asp Asp Gln Met Lys Leu Leu Gln Asn Cys
115 120 125
Trp Ser Glu Leu Leu Ile Leu Asp His Ile Thr Arg Gln Val Ala His
130 135 140
Gly Lys Glu Gly Thr Ile Phe Leu Val Thr Gly Glu His Val Asp Tyr
145 150 155 160
Ser Thr Ile Ile Ser His Thr Glu Val Ala Arg Asn Asn Leu Leu Ser
165 170 175
Leu Ala Gln Glu Leu Val Val Arg Leu Arg Ser Leu Gln Glu Asp Gln
180 185 190
Arg Glu Glu Val Cys Leu Lys Phe Leu Val Leu Phe Ser Ser Asp Val
195 200 205
Phe Asn Leu Glu Asn Leu Gln Leu Val Glu Gly Val Gln Glu Gln Val
210 215 220
Asn Ala Ala Leu Leu Asp Tyr Thr Val Cys Asn Tyr Pro Gln Gln Thr
225 230 235 240
Glu Lys Phe Gly Gln Leu Leu Leu Arg Leu Pro Glu Ile Arg Ala Ile
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Ser Lys Gln Ala Glu Asp Tyr Leu Tyr Tyr Lys His Val Asn Gly Asp
260 265 270
Val Pro Tyr Met Asn Leu Leu Ile Glu Met Leu His Ala Lys Arg Ala
275 280 285

<210> 4
<211> 286
<212> PRT
<213> Homo sapiens

<400> 4
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Tyr	Ser	Tyr	Met	Asp	Ser	Tyr	Gln	Thr	Ser	Ser	Pro	Ala	Ser	Ile	Pro
		35					40					45			
His	Leu	Ile	Leu	Glu	Leu	Leu	Lys	Cys	Glu	Pro	Asp	Glu	Pro	Gln	Val
	50					55					60				
Gln	Ala	Lys	Ile	Met	Ala	Tyr	Leu	Gln	Gln	Glu	Gln	Ala	Asn	Arg	Ser
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Lys	His	Glu	Lys	Leu	Ser	Thr	Phe	Gly	Ile	Met	Cys	Arg	Met	Ala	Asp
			85					90						95	
Gln	Thr	Leu	Phe	Ser	Ile	Val	Glu	Trp	Ala	Arg	Ser	Ser	Ile	Phe	Phe
			100					105					110		
Arg	Glu	Leu	Lys	Val	Asp	Asp	Gln	Met	Lys	Leu	Leu	Gln	Asn	Cys	Trp
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Ser	Glu	Leu	Leu	Ile	Leu	Asp	His	Ile	Tyr	Arg	Gln	Val	Val	His	Gly
	130					135					140				
Lys	Glu	Gly	Ser	Ile	Phe	Leu	Val	Thr	Gly	Gln	Gln	Val	Asp	Tyr	Ser
145					150					155					160
Ile	Ile	Ala	Ser	Gln	Ala	Gly	Ala	Thr	Ile	Asn	Asn	Ile	Met	Ser	His
				165					170						175
Ala	Gln	Glu	Leu	Val	Lys	Leu	Arg	Ser	Leu	Gln	Glu	Asp	Gln	Arg	Glu
			180					185					190		
Phe	Val	Cys	Leu	Lys	Phe	Leu	Val	Leu	Phe	Ser	Leu	Asp	Val	Phe	Asn
		195					200					205			
Leu	Glu	Asn	Phe	Gln	Leu	Val	Glu	Gly	Val	Gln	Glu	Gln	Val	Asn	Ala
	210					215					220				
Ala	Leu	Leu	Asp	Tyr	Thr	Met	Cys	Asn	Tyr	Pro	Gln	Gln	Thr	Glu	Lys
225					230					235					240
Phe	Gly	Gln	Leu	Leu	Leu	Arg	Leu	Pro	Glu	Ile	Arg	Ala	Ile	Ser	Met
				245					250					255	
Gln	Ala	Glu	Glu	Tyr	Leu	Tyr	Tyr	Lys	His	Ile	Asn	Gly	Asp	Val	Pro
			260					265					270		
Tyr	Asn	Asn	Leu	Leu	Ile	Glu	Met	Leu	His	Ala	Lys	Arg	Ala		
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<211> 260

<212> PRT

<213> Homo sapiens

<400> 5

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			20					25					30		
Glu	Arg	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Val	Glu	Pro	Lys	Thr	Glu	Thr
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Tyr	Val	Glu	Ala	Asn	Met	Gly	Ile	Asn	Pro	Ser	Ser	Pro	Asn	Asp	Pro
	50					55					60				
Val	Thr	Asn	Ile	Cys	Gln	Ala	Ala	Asp	Lys	Gln	Leu	Phe	Thr	Leu	Val
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Glu	Trp	Ala	Lys	Arg	Ile	Pro	His	Phe	Ser	Glu	Leu	Pro	Leu	Asp	Asp

<213> Mus musculus

<222> (1) ... (1389)

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Gly Asp Lys Val Ser Gly Tyr His Tyr Gly Leu Leu Thr Cys Glu Ser
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tgc aag ggc ttc ttc aag cgc aca gtc cag aac aac aag cat tac acg 144
Cys Lys Gly Phe Phe Lys Arg Thr Val Gln Asn Asn Lys His Tyr Thr
35 40 45

tgc acc gag agt cag agc tgc aaa atc gac aag acg cag cgt aag cgc 192
Cys Thr Glu Ser Gln Ser Cys Lys Ile Asp Lys Thr Gln Arg Lys Arg
50 55 60

tgt ccc ttc tgc cgc ttc cag aag tgc ctg acg gtg ggc atg cgc ctg 240
Cys Pro Phe Cys Arg Phe Gln Lys Cys Leu Thr Val Gly Met Arg Leu

65	70					75					80					
gaa gct gtg cgt gct gat cga atg cgg ggt ggc cgg aac aag ttt ggg	288															
Glu Ala Val Arg Ala Asp Arg Met Arg Gly Gly Arg Asn Lys Phe Gly																
	85					90					95					
ccc atg tac aag aga gac cgg gcc ttg aag cag cag aag aaa gca cag	336															
Pro Met Tyr Lys Arg Asp Arg Ala Leu Lys Gln Gln Lys Lys Ala Gln																
	100					105					110					
att cgg gcc aat ggc ttc aag ctg gag acc gga cca ccg atg ggg gtg	384															
Ile Arg Ala Asn Gly Phe Lys Leu Glu Thr Gly Pro Pro Met Gly Val																
	115					120					125					
ccc ccg cca ccc cct ccc cca ccg gac tac atg tta ccc cct agc ctg	432															
Pro Pro Pro Pro Pro Pro Pro Pro Asp Tyr Met Leu Pro Pro Ser Leu																
	130					135					140					
cac gca ccg gag ccc aag gcc ctg gtc tct ggc cca ccc agt ggg ccg	480															
His Ala Pro Glu Pro Lys Ala Leu Val Ser Gly Pro Pro Ser Gly Pro																
	145					150					155					
ctg ggt gac ttt gga gcc cca tct cta ccc atg gct gtg cct ggt ccc	528															
Leu Gly Asp Phe Gly Ala Pro Ser Leu Pro Met Ala Val Pro Gly Pro																
	165					170					175					
cac gga cct ctg gct ggc tac ctc tat cct gcc ttc tct aac cgc acc	576															
His Gly Pro Leu Ala Gly Tyr Leu Tyr Pro Ala Phe Ser Asn Arg Thr																
	180					185					190					
atc aag tct gag tat cca gag ccc tat gcc agc ccc cca caa cag cca	624															
Ile Lys Ser Glu Tyr Pro Glu Pro Tyr Ala Ser Pro Pro Gln Gln Pro																
	195					200					205					
ggg cca ccc tac agc tat cca gag ccc ttc tca gga ggg ccc aat gta	672															
Gly Pro Pro Tyr Ser Tyr Pro Glu Pro Phe Ser Gly Gly Pro Asn Val																
	210					215					220					
cca gag ctc ata ttg cag ctg ctg caa cta gag cca gag gag gac cag	720															
Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu Glu Pro Glu Glu Asp Gln																
	225					230					235					
gtg cgc gct cgc atc gtg ggc tgt ctg cag gag cca gcc aaa agc cgc	768															
Val Arg Ala Arg Ile Val Gly Cys Leu Gln Glu Pro Ala Lys Ser Arg																
	245					250					255					
tct gac cag cca gcg ccc ttc agc ctc ctc tgc aga atg gcc gac cag	816															
Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu Cys Arg Met Ala Asp Gln																
	260					265					270					
acc ttt atc tcc att gtc gac tgg gca cga agg tgc atg gtc ttt aag	864															
Thr Phe Ile Ser Ile Val Asp Trp Ala Arg Arg Cys Met Val Phe Lys																
	275					280					285					

gag ctg gag gtg gct gac cag atg aca ctg ctg cag aac tgt tgg agc	912
Glu Leu Glu Val Ala Asp Gln Met Thr Leu Leu Gln Asn Cys Trp Ser	
290 295 300	
gag ctg ctg gtg ttg gac cac atc tac cgc cag gtc cag tac ggc aag	960
Glu Leu Leu Val Leu Asp His Ile Tyr Arg Gln Val Gln Tyr Gly Lys	
305 310 315 320	
gaa gac agc atc ctg ctg gtt act gga cag gag gtg gag ctg agc aca	1008
Glu Asp Ser Ile Leu Leu Val Thr Gly Gln Glu Val Glu Leu Ser Thr	
325 330 335	
gtg gct gtg cag gct ggc tcc ctg ctg cac agc ctg gtg ctg cgg gcc	1056
Val Ala Val Gln Ala Gly Ser Leu Leu His Ser Leu Val Leu Arg Ala	
340 345 350	
caa gag tta gtg ctc cag ttg cat gca ctg cag ctg gac cgc cag gag	1104
Gln Glu Leu Val Leu Gln Leu His Ala Leu Gln Leu Asp Arg Gln Glu	
355 360 365	
ttc gtc tgt ctc aag ttc ctc atc ctc ttc agc ctc gat gtg aaa ttc	1152
Phe Val Cys Leu Lys Phe Leu Ile Leu Phe Ser Leu Asp Val Lys Phe	
370 375 380	
ctg aac aac cac agc ctc gta aag gac gcc cag gaa aag gcc aac gct	1200
Leu Asn Asn His Ser Leu Val Lys Asp Ala Gln Glu Lys Ala Asn Ala	
385 390 395 400	
gcc ctg ttg gat tac acc ttg tgt cac tac cca cac tgc ggg gac aaa	1248
Ala Leu Leu Asp Tyr Thr Leu Cys His Tyr Pro His Cys Gly Asp Lys	
405 410 415	
ttc cag cag ttg cta ttg tgc ctg gtg gag gtg cgg gcc ctg agc atg	1296
Phe Gln Gln Leu Leu Leu Cys Leu Val Glu Val Arg Ala Leu Ser Met	
420 425 430	
cag gcc aag gag tac ctg tac cac aag cat ttg ggc aac gag atg ccc	1344
Gln Ala Lys Glu Tyr Leu Tyr His Lys His Leu Gly Asn Glu Met Pro	
435 440 445	
cgc aac aac ctt ctc att gag atg ctg cag gcc aag cag act tga	1389
Arg Asn Asn Leu Leu Ile Glu Met Leu Gln Ala Lys Gln Thr *	
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<210> 7

<211> 462

<212> PRT

<213> Mus musculus

<400> 7

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Cys	Lys	Gly	Phe	Phe	Lys	Arg	Thr	Val	Gln	Asn	Asn	Lys	His	Tyr	Thr
		35					40					45			
Cys	Thr	Glu	Ser	Gln	Ser	Cys	Lys	Ile	Asp	Lys	Thr	Gln	Arg	Lys	Arg
	50					55					60				
Cys	Pro	Phe	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Thr	Val	Gly	Met	Arg	Leu
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Glu	Ala	Val	Arg	Ala	Asp	Arg	Met	Arg	Gly	Gly	Arg	Asn	Lys	Phe	Gly
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Pro	Met	Tyr	Lys	Arg	Asp	Arg	Ala	Leu	Lys	Gln	Gln	Lys	Lys	Ala	Gln
			100					105					110		
Ile	Arg	Ala	Asn	Gly	Phe	Lys	Leu	Glu	Thr	Gly	Pro	Pro	Met	Gly	Val
		115					120					125			
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Asp	Tyr	Met	Leu	Pro	Pro	Ser	Leu
	130					135					140				
His	Ala	Pro	Glu	Pro	Lys	Ala	Leu	Val	Ser	Gly	Pro	Pro	Ser	Gly	Pro
145				150						155					160
Leu	Gly	Asp	Phe	Gly	Ala	Pro	Ser	Leu	Pro	Met	Ala	Val	Pro	Gly	Pro
				165					170					175	
His	Gly	Pro	Leu	Ala	Gly	Tyr	Leu	Tyr	Pro	Ala	Phe	Ser	Asn	Arg	Thr
			180					185					190		
Ile	Lys	Ser	Glu	Tyr	Pro	Glu	Pro	Tyr	Ala	Ser	Pro	Pro	Gln	Gln	Pro
		195					200					205			
Gly	Pro	Pro	Tyr	Ser	Tyr	Pro	Glu	Pro	Phe	Ser	Gly	Gly	Pro	Asn	Val
	210					215					220				
Pro	Glu	Leu	Ile	Leu	Gln	Leu	Leu	Gln	Leu	Glu	Pro	Glu	Glu	Asp	Gln
225				230						235					240
Val	Arg	Ala	Arg	Ile	Val	Gly	Cys	Leu	Gln	Glu	Pro	Ala	Lys	Ser	Arg
				245					250					255	
Ser	Asp	Gln	Pro	Ala	Pro	Phe	Ser	Leu	Leu	Cys	Arg	Met	Ala	Asp	Gln
			260					265					270		
Thr	Phe	Ile	Ser	Ile	Val	Asp	Trp	Ala	Arg	Arg	Cys	Met	Val	Phe	Lys
		275					280					285			
Glu	Leu	Glu	Val	Ala	Asp	Gln	Met	Thr	Leu	Leu	Gln	Asn	Cys	Trp	Ser
	290					295					300				
Glu	Leu	Leu	Val	Leu	Asp	His	Ile	Tyr	Arg	Gln	Val	Gln	Tyr	Gly	Lys
305				310					315						320
Glu	Asp	Ser	Ile	Leu	Leu	Val	Thr	Gly	Gln	Glu	Val	Glu	Leu	Ser	Thr
				325					330					335	
Val	Ala	Val	Gln	Ala	Gly	Ser	Leu	Leu	His	Ser	Leu	Val	Leu	Arg	Ala
			340					345					350		
Gln	Glu	Leu	Val	Leu	Gln	Leu	His	Ala	Leu	Gln	Leu	Asp	Arg	Gln	Glu

	420		425		430										
Gln	Ala	Lys	Glu	Tyr	Leu	Tyr	His	Lys	His	Leu	Gly	Asn	Glu	Met	Pro
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (16)...(1401)

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 Cys Pro Val Cys Gly Asp Lys Val Ser Gly Tyr His Tyr Gly Leu Leu
 15 20 25

acg tgt gag agc tgc aag ggc ttc ttc aag cgc acg gtg cag aac aac 147
 Thr Cys Glu Ser Cys Lys Gly Phe Phe Lys Arg Thr Val Gln Asn Asn
 30 35 40

aag cac tac acg tgc acc gag agc cag agc tgc aag atc gac aag acg 195
 Lys His Tyr Thr Cys Thr Glu Ser Gln Ser Cys Lys Ile Asp Lys Thr
 45 50 55 60

cag cgc aag cgc tgt ccc ttc tgc cgc ttc cag aaa tgc ctg acg gtg 243
 Gln Arg Lys Arg Cys Pro Phe Cys Arg Phe Gln Lys Cys Leu Thr Val
 65 70 75

ggg atg cgc ctg gaa gcc gtg cgc gct gac cgt atg agg ggt ggc cgg 291
 Gly Met Arg Leu Glu Ala Val Arg Ala Asp Arg Met Arg Gly Gly Arg
 80 85 90

aac aag ttt ggg ccg atg tac aag cgg gac cgg gcc ctg aaa cag cag 339
 Asn Lys Phe Gly Pro Met Tyr Lys Arg Asp Arg Ala Leu Lys Gln Gln
 95 100 105

aag aag gca cag att cgg gcc aat ggc ttc aag ctg gag aca ggg ccc 387
 Lys Lys Ala Gln Ile Arg Ala Asn Gly Phe Lys Leu Glu Thr Gly Pro
 110 115 120

ccg atg ggg gtg ccc ccg ccg ccc cct ccc gca ccg gac tac gtg ctg 435
 Pro Met Gly Val Pro Pro Pro Pro Pro Pro Ala Pro Asp Tyr Val Leu
 125 130 135 140

cct ccc agc ctg cat ggg cct gag ccc aag ggc ctg gcc gcc ggt cca	483
Pro Pro Ser Leu His Gly Pro Glu Pro Lys Gly Leu Ala Ala Gly Pro	
145 150 155	
cct gct ggg cca ctg ggc gac ttt ggg gcc cca gca ctg ccc atg gcc	531
Pro Ala Gly Pro Leu Gly Asp Phe Gly Ala Pro Ala Leu Pro Met Ala	
160 165 170	
gtg ccc ggt gcc cac ggg cca ctg gct ggc tac ctc tac cct gcc ttt	579
Val Pro Gly Ala His Gly Pro Leu Ala Gly Tyr Leu Tyr Pro Ala Phe	
175 180 185	
cct ggc cgt gcc atc aag tct gag tac ccg gag cct tat gcc agc ccc	627
Pro Gly Arg Ala Ile Lys Ser Glu Tyr Pro Glu Pro Tyr Ala Ser Pro	
190 195 200	
cca cag cct ggg ctg ccg tac ggc tac cca gag ccc ttc tct gga ggc	675
Pro Gln Pro Gly Leu Pro Tyr Gly Tyr Pro Glu Pro Phe Ser Gly Gly	
205 210 215 220	
ccc aac gtg cct gag ctc atc ctg cag ctg ctg cag ctg gag ccg gat	723
Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu Glu Pro Asp	
225 230 235	
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Glu Asp Gln Val Arg Ala Arg Ile Leu Gly Cys Leu Gln Glu Pro Thr	
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Lys Ser Arg Pro Asp Gln Pro Ala Ala Phe Gly Leu Leu Cys Arg Met	
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Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu Leu Gln Asn	
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Cys Trp Ser Glu Leu Leu Val Phe Asp His Ile Tyr Arg Gln Val Gln	
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His Gly Lys Glu Gly Ser Ile Leu Leu Val Thr Gly Gln Glu Val Glu	
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Leu Thr Thr Val Ala Thr Gln Ala Gly Ser Leu Leu His Ser Leu Val	
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 Gly Asp Lys Phe Gln Gln Leu Leu Leu Cys Leu Val Glu Val Arg Ala
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Val	Cys	Leu	Lys	Phe	Ile	Ile	Leu	Phe	Ser	Leu	Asp	Leu	Lys	Phe	Leu		
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Asn	Asn	His	Ile	Leu	Val	Lys	Asp	Ala	Gln	Glu	Lys	Ala	Asn	Ala	Ala		
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Gln	Gln	Leu	Leu	Leu	Cys	Leu	Val	Glu	Val	Arg	Ala	Leu	Ser	Met	Gln		
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Thr Gly Asp Phe Gln Glu Phe Leu Lys His Gly Leu Thr Ala Ile Ala
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Ser Ala Pro Gly Ser Glu Thr Arg His Ser Pro Lys Arg Glu Glu Gln
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ctc cgg gaa aaa cgt gct ggg ctt ccg gac cga cac cga cgc ccc att 320
Leu Arg Glu Lys Arg Ala Gly Leu Pro Asp Arg His Arg Arg Pro Ile
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ccc gcc cgc agc cgc ctt gtc atg ctg ccc aaa gtg gag acg gaa gcc 368
Pro Ala Arg Ser Arg Leu Val Met Leu Pro Lys Val Glu Thr Glu Ala
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cca gga ctg gtc cga tcg cat ggg gaa cag ggg cag atg cca gaa aac 416
Pro Gly Leu Val Arg Ser His Gly Glu Gln Gly Gln Met Pro Glu Asn
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Met Gln Val Ser Gln Phe Lys Met Val Asn Tyr Ser Tyr Asp Glu Asp
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Val Gln Asn Gln Lys Arg Tyr Thr Cys Ile Glu Asn Gln Asn Cys Gln
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Glu	Ala	Met	Ser	Gln	Val	Ile	Gln	Ala	Met	Pro	Ser	Asp	Leu	Thr	Ser		
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Val	Ala	Leu	Pro	Pro	Thr	Asp	Tyr	Asp	Arg	Ser	Pro	Phe	Val	Thr	Ser		
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Val Arg Leu Arg Ser Leu Gln Phe Asp Gln Arg Glu Phe Val Cys Leu			
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Lys Phe Leu Val Leu Phe Ser Ser Asp Val Lys Asn Leu Glu Asn Leu			
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Glu Asp Leu Glu Glu Leu Cys Pro Val Cys Gly Asp Lys Val Ser Gly	
35 40 45	
tac cat tat ggg ctc ctc acc tgt gaa agc tgc aag gga ttt ttt aag	250
Tyr His Tyr Gly Leu Leu Thr Cys Glu Ser Cys Lys Gly Phe Phe Lys	
50 55 60 65	
cga aca gtc caa aat aat aaa agg tac aca tgt ata gaa aac cag aac	298
Arg Thr Val Gln Asn Asn Lys Arg Tyr Thr Cys Ile Glu Asn Gln Asn	
70 75 80	
tgc caa att gac aaa aca cag aga aag cgt tgt cct tac tgt cgt ttt	346
Cys Gln Ile Asp Lys Thr Gln Arg Lys Arg Cys Pro Tyr Cys Arg Phe	
85 90 95	
caa aaa tgt cta agt gtt gga atg aag cta gaa gct gta agg gcc gac	394
Gln Lys Cys Leu Ser Val Gly Met Lys Leu Glu Ala Val Arg Ala Asp	
100 105 110	
cga atg cgt gga gga agg aat aag ttt ggg cca atg tac aag aga gac	442
Arg Met Arg Gly Gly Arg Asn Lys Phe Gly Pro Met Tyr Lys Arg Asp	
115 120 125	
agg gcc ctg aag caa cag aaa aaa gcc ctc atc cga gcc aat gga ctt	490
Arg Ala Leu Lys Gln Gln Lys Lys Ala Leu Ile Arg Ala Asn Gly Leu	
130 135 140 145	
aag cta gaa gcc atg tct cag gtg atc caa gct atg ccc tct gac ctg	538
Lys Leu Glu Ala Met Ser Gln Val Ile Gln Ala Met Pro Ser Asp Leu	
150 155 160	
acc att tcc tct gca att caa aac atc cac tct gcc tcc aaa ggc cta	586
Thr Ile Ser Ser Ala Ile Gln Asn Ile His Ser Ala Ser Lys Gly Leu	
165 170 175	
cct ctg aac cat gct gcc ttg cct cct aca gac tat gac aga agt ccc	634
Pro Leu Asn His Ala Ala Leu Pro Pro Thr Asp Tyr Asp Arg Ser Pro	
180 185 190	
ttt gta aca tcc ccc att agc atg aca atg ccc cct cac ggc agc ctg	682

Phe	Val	Thr	Ser	Pro	Ile	Ser	Met	Thr	Met	Pro	Pro	His	Gly	Ser	Leu		
195						200				205							
caa	ggt	tac	caa	aca	tat	ggc	cac	ttt	cct	agc	cgg	gcc	atc	aag	tct	730	
Gln	Gly	Tyr	Gln	Thr	Tyr	Gly	His	Phe	Pro	Ser	Arg	Ala	Ile	Lys	Ser		
210					215				220					225			
gag	tac	cca	gac	ccc	tat	acc	agc	tca	ccc	gag	tcc	ata	atg	ggc	tat	778	
Glu	Tyr	Pro	Asp	Pro	Tyr	Thr	Ser	Ser	Pro	Glu	Ser	Ile	Met	Gly	Tyr		
				230					235					240			
tca	tat	atg	gat	agt	tac	cag	acg	agc	tct	cca	gca	agc	atc	cca	cat	826	
Ser	Tyr	Met	Asp	Ser	Tyr	Gln	Thr	Ser	Ser	Pro	Ala	Ser	Ile	Pro	His		
				245				250					255				
ctg	ata	ctg	gaa	ctt	ttg	aag	tgt	gag	cca	gat	gag	cct	caa	gtc	cag	874	
Leu	Ile	Leu	Glu	Leu	Leu	Lys	Cys	Glu	Pro	Asp	Glu	Pro	Gln	Val	Gln		
	260					265						270					
gct	aaa	atc	atg	gcc	tat	ttg	cag	caa	gag	cag	gct	aac	cga	agc	aag	922	
Ala	Lys	Ile	Met	Ala	Tyr	Leu	Gln	Gln	Glu	Gln	Ala	Asn	Arg	Ser	Lys		
	275					280					285						
cac	gaa	aag	ctg	agc	acc	ttt	ggg	ctt	atg	tgc	aaa	atg	gca	gat	caa	970	
His	Glu	Lys	Leu	Ser	Thr	Phe	Gly	Leu	Met	Cys	Lys	Met	Ala	Asp	Gln		
290					295					300					305		
act	ctc	ttc	tcc	att	gtc	gag	tgg	gcc	agg	agt	agt	atc	ttc	ttc	aga	1018	
Thr	Leu	Phe	Ser	Ile	Val	Glu	Trp	Ala	Arg	Ser	Ser	Ile	Phe	Phe	Arg		
				310				315						320			
gaa	ctt	aag	gtt	gat	gac	caa	atg	aag	ctg	ctt	cag	aac	tgc	tgg	agt	1066	
Glu	Leu	Lys	Val	Asp	Asp	Gln	Met	Lys	Leu	Leu	Gln	Asn	Cys	Trp	Ser		
			325					330					335				
gag	ctc	tta	atc	ctc	gac	cac	att	tac	cga	caa	gtg	gta	cat	gga	aag	1114	
Glu	Leu	Leu	Ile	Leu	Asp	His	Ile	Tyr	Arg	Gln	Val	Val	His	Gly	Lys		
		340					345					350					
gaa	gga	tcc	atc	ttc	ctg	gtt	act	ggg	caa	caa	gtg	gac	tat	tcc	ata	1162	
Glu	Gly	Ser	Ile	Phe	Leu	Val	Thr	Gly	Gln	Gln	Val	Asp	Tyr	Ser	Ile		
	355					360					365						
ata	gca	tca	caa	gcc	gga	gcc	acc	ctc	aac	aac	ctc	atg	agt	cat	gca	1210	
Ile	Ala	Ser	Gln	Ala	Gly	Ala	Thr	Leu	Asn	Asn	Leu	Met	Ser	His	Ala		
370					375					380					385		
cag	gag	tta	gtg	gca	aaa	ctt	cgt	tct	ctc	cag	ttt	gat	caa	cga	gag	1258	
Gln	Glu	Leu	Val	Ala	Lys	Leu	Arg	Ser	Leu	Gln	Phe	Asp	Gln	Arg	Glu		
			390					395					400				
ttc	gta	tgt	ctg	aaa	ttc	ttg	gtg	ctc	ttt	agt	tta	gat	gtc	aaa	aac	1306	
Phe	Val	Cys	Leu	Lys	Phe	Leu	Val	Leu	Phe	Ser	Leu	Asp	Val	Lys	Asn		

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405              410              415
ctt gaa aac ttc cag ctg gta gaa ggt gtc cag gaa caa gtc aat gcc 1354
Leu Glu Asn Phe Gln Leu Val Glu Gly Val Gln Glu Gln Val Asn Ala
      420              425              430

gcc ctg ctg gac tac aca atg tgt aac tac ccg cag cag aca gag aaa 1402
Ala Leu Leu Asp Tyr Thr Met Cys Asn Tyr Pro Gln Gln Thr Glu Lys
      435              440              445

ttt gga cag cta ctt ctt cga cta ccc gaa atc cgg gcc atc agt atg 1450
Phe Gly Gln Leu Leu Arg Leu Pro Glu Ile Arg Ala Ile Ser Met
450              455              460              465

cag gct gaa gaa tac ctc tac tac aag cac ctg aac ggg gat gtg ccc 1498
Gln Ala Glu Glu Tyr Leu Tyr Tyr Lys His Leu Asn Gly Asp Val Pro
      470              475              480

tat aat aac ctt ctc att gaa atg ttg cat gcc aaa aga gca taa 1543
Tyr Asn Asn Leu Leu Ile Glu Met Leu His Ala Lys Arg Ala *
      485              490              495

gttacaaccc ctaggagctc tgctttcaaa acaaaaagag attgggggag tggggaggggg 1603
gaagaagaac aggaagaaaa aaagtactct gaactgctcc aagcaacgct aattaaaaaac 1663
ttgctttaaa gatattgaat ttaaaaaggc ataataatca aataacttaat agcaaataaaa 1723
tgatgtatca gggtatattgt attgcaaact gtgaatcaaa ggcttcacag cccagagga 1783
ttccatataa aagacattgt aaggagtggg ttgaactcac agatggatac caacacggtc 1843
agaagaaaaa cggacagaac ggttcttgta tattaaactg atctccacta tgaagaaatt 1903
taggaactaa tcttgtaaat taggcttata cagcggggga tttgagctta caggattcct 1963
ccatggtaaa gctgaactga aacaattctc aagaatgcat cagctgtacc tacaatagcc 2023
cctccctctt cctttgaagg cccgagcacc tctgcctgtt ggtcaccgaa tctgtactaa 2083
ggacctgtgt tcagccacac cagtggtagc tccaccaaatt catgaacagc ctaatttgag 2143
tgtctgtgtc ttagacctgc aaacagctaa taggaaattc tattaatatg ttagcttgcc 2203
attttaaata tgttctgagg gttgttttgt ctcgtgttca tgatgttaag aaaatgcagg 2263
cagtatccct catcttatgt aagtgtgaat taatattaag ggaaatgact acaaactttc 2323
aaagcaaatg ctccatagct aaagcaactt agaccttatt tctgctactg ttgctgaaat 2383
gtggctttgg cattgttgga tttcataaaa aatttctggc aggaagtctt gttagtatac 2443
atcagtcttt ttcacatccc aagttttagt ttcatttaa 2482

<210> 13
<211> 495
<212> PRT
<213> Homo sapiens

<400> 13
Met Ser Ser Asn Ser Asp Thr Gly Asp Leu Gln Glu Ser Leu Lys His
 1          5          10         15
Gly Leu Thr Pro Ile Val Ser Gln Phe Lys Met Val Asn Tyr Ser Tyr
      20          25          30
Asp Glu Asp Leu Glu Glu Leu Cys Pro Val Cys Gly Asp Lys Val Ser
      35          40          45
Gly Tyr His Tyr Gly Leu Leu Thr Cys Glu Ser Cys Lys Gly Phe Phe
      50          55          60
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Lys	Arg	Thr	Val	Gln	Asn	Asn	Lys	Arg	Tyr	Thr	Cys	Ile	Glu	Asn	Gln	65	70	75	80
Asn	Cys	Gln	Ile	Asp	Lys	Thr	Gln	Arg	Lys	Arg	Cys	Pro	Tyr	Cys	Arg	85	90	95	
Phe	Gln	Lys	Cys	Leu	Ser	Val	Gly	Met	Lys	Leu	Glu	Ala	Val	Arg	Ala	100	105	110	
Asp	Arg	Met	Arg	Gly	Gly	Arg	Asn	Lys	Phe	Gly	Pro	Met	Tyr	Lys	Arg	115	120	125	
Asp	Arg	Ala	Leu	Lys	Gln	Gln	Lys	Lys	Ala	Leu	Ile	Arg	Ala	Asn	Gly	130	135	140	
Leu	Lys	Leu	Glu	Ala	Met	Ser	Gln	Val	Ile	Gln	Ala	Met	Pro	Ser	Asp	145	150	155	160
Leu	Thr	Ile	Ser	Ser	Ala	Ile	Gln	Asn	Ile	His	Ser	Ala	Ser	Lys	Gly	165	170	175	
Leu	Pro	Leu	Asn	His	Ala	Ala	Leu	Pro	Pro	Thr	Asp	Tyr	Asp	Arg	Ser	180	185	190	
Pro	Phe	Val	Thr	Ser	Pro	Ile	Ser	Met	Thr	Met	Pro	Pro	His	Gly	Ser	195	200	205	
Leu	Gln	Gly	Tyr	Gln	Thr	Tyr	Gly	His	Phe	Pro	Ser	Arg	Ala	Ile	Lys	210	215	220	
Ser	Glu	Tyr	Pro	Asp	Pro	Tyr	Thr	Ser	Ser	Pro	Glu	Ser	Ile	Met	Gly	225	230	235	240
Tyr	Ser	Tyr	Met	Asp	Ser	Tyr	Gln	Thr	Ser	Ser	Pro	Ala	Ser	Ile	Pro	245	250	255	
His	Leu	Ile	Leu	Glu	Leu	Leu	Lys	Cys	Glu	Pro	Asp	Glu	Pro	Gln	Val	260	265	270	
Gln	Ala	Lys	Ile	Met	Ala	Tyr	Leu	Gln	Gln	Glu	Gln	Ala	Asn	Arg	Ser	275	280	285	
Lys	His	Glu	Lys	Leu	Ser	Thr	Phe	Gly	Leu	Met	Cys	Lys	Met	Ala	Asp	290	295	300	
Gln	Thr	Leu	Phe	Ser	Ile	Val	Glu	Trp	Ala	Arg	Ser	Ser	Ile	Phe	Phe	305	310	315	320
Arg	Glu	Leu	Lys	Val	Asp	Asp	Gln	Met	Lys	Leu	Leu	Gln	Asn	Cys	Trp	325	330	335	
Ser	Glu	Leu	Leu	Ile	Leu	Asp	His	Ile	Tyr	Arg	Gln	Val	Val	His	Gly	340	345	350	
Lys	Glu	Gly	Ser	Ile	Phe	Leu	Val	Thr	Gly	Gln	Gln	Val	Asp	Tyr	Ser	355	360	365	
Ile	Ile	Ala	Ser	Gln	Ala	Gly	Ala	Thr	Leu	Asn	Asn	Leu	Met	Ser	His	370	375	380	
Ala	Gln	Glu	Leu	Val	Ala	Lys	Leu	Arg	Ser	Leu	Gln	Phe	Asp	Gln	Arg	385	390	395	400
Glu	Phe	Val	Cys	Leu	Lys	Phe	Leu	Val	Leu	Phe	Ser	Leu	Asp	Val	Lys	405	410	415	
Asn	Leu	Glu	Asn	Phe	Gln	Leu	Val	Glu	Gly	Val	Gln	Glu	Gln	Val	Asn	420	425	430	
Ala	Ala	Leu	Leu	Asp	Tyr	Thr	Met	Cys	Asn	Tyr	Pro	Gln	Gln	Thr	Glu	435	440	445	
Lys	Phe	Gly	Gln	Leu	Leu	Leu	Arg	Leu	Pro	Glu	Ile	Arg	Ala	Ile	Ser	450	455	460	
Met	Gln	Ala	Glu	Glu	Tyr	Leu	Tyr	Tyr	Lys	His	Leu	Asn	Gly	Asp	Val	465	470	475	480
Pro	Tyr	Asn	Asn	Leu	Leu	Ile	Glu	Met	Leu	His	Ala	Lys	Arg	Ala					

485

490

495

<210> 14
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic variant

<221> CDS
<222> (1)...(735)

<400> 14
tca gga ggg ccc aat gta cca gag ctc ata ttg cag ctg ctg caa cta 48
Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu
1 5 10 15

gag cca gag gag gac cag gtg cgc gct cgc atc gtg ggc tgt ctg cag 96
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln
20 25 30

gag cca gcc aaa agc cgc tct gac cag cca gcg ccc ttc agc ctc ctc 144
Glu Pro Ala Lys Ser Arg Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu
35 40 45

tcg cga atg gcc gac cag acc ttt atc tcc att gtc gac tgg gca cga 192
Ser Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg
50 55 60

agg tgc atg gtc ttt aag gag ctg gag gtg gct gac cag atg aca ctg 240
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu
65 70 75 80

ctg caa aac tct tgg agc gag ctg ctg gtg ttg gac cac atc tac cgc 288
Leu Gln Asn Ser Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg
85 90 95

cag gtc cag tac ggc aag gaa gac agc atc ctg ctg gtt act gga cag 336
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln
100 105 110

gag gtg gag ctg agc aca gtg gct gtg cag gct ggc tcc ctg ctg cac 384
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His
115 120 125

agc ctg gtg ctg cgg gcc caa gag tta gtg ctc cag ttg cat gca ctg 432
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu
130 135 140

cag ctg gac cgc cag gag ttc gtc tgt ctc aag ttc ctc atc ctc ttc 480
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe

145	150	155	160	
agc ctc gat gtg aaa ttc ctg aac aac cac agc ctc gta aag gac gcc				528
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala				
	165	170	175	
cag gaa aag gcc aac gct gcc ctg ttg gat tac acc ttg tgt cac tac				576
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Cys His Tyr				
	180	185	190	
cca cac tgc ggg gac aaa ttc cag cag ttg cta ttg tcg ctg gtg gag				624
Pro His Cys Gly Asp Lys Phe Gln Gln Leu Leu Ser Leu Val Glu				
	195	200	205	
gtg cgg gcc ctg agc atg cag gcc aag gag tac ctg tac cac aag cat				672
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His				
	210	215	220	
ttg ggc aac gag atg ccc cgc aac aac ctt ctc att gag atg ctg cag				720
Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln				
	225	230	235	240
gcc aag cag act tga				735
Ala Lys Gln Thr *				

<210> 15

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic variant

<400> 15

Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu				
1	5	10	15	
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln				
	20	25	30	
Glu Pro Ala Lys Ser Arg Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu				
	35	40	45	
Ser Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg				
	50	55	60	
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu				
	65	70	75	80
Leu Gln Asn Ser Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg				
	85	90	95	
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln				
	100	105	110	
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His				
	115	120	125	
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu				

130		135		140	
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe					
145		150		155	160
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala					
	165		170		175
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Cys His Tyr					
	180		185		190
Pro His Cys Gly Asp Lys Phe Gln Gln Leu Leu Leu Ser Leu Val Glu					
	195		200		205
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His					
	210		215		220
Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln					
225		230		235	240
Ala Lys Gln Thr					

<210> 16

<211> 735

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic variant

<221> CDS

<222> (1)...(735)

<400> 16

tca gga ggg ccc aat gta cca gag ctc ata ttg cag ctg ctg caa cta	48
Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu	
1 5 10 15	

gag cca gag gag gac cag gtg cgc gct cgc atc gtg ggc tgt ctg cag	96
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln	
20 25 30	

gag cca gcc aaa agc cgc tct gac cag cca gcg ccc ttc agc ctc ctc	144
Glu Pro Ala Lys Ser Arg Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu	
35 40 45	

tgc aga atg gcc gac cag acc ttt atc tcc att gtc gac tgg gca cga	192
Cys Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg	
50 55 60	

agg tgc atg gtc ttt aag gag ctg gag gtg gct gac cag atg aca ctg	240
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu	
65 70 75 80	

ctg caa aac tct tgg agc gag ctg ctg gtg ttg gac cac atc tac cgc	288
Leu Gln Asn Ser Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg	
85 90 95	

cag gtc cag tac ggc aag gaa gac agc atc ctg ctg gtt act gga cag	336
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln	
100 105 110	
gag gtg gag ctg agc aca gtg gct gtg cag gct ggc tcc ctg ctg cac	384
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His	
115 120 125	
agc ctg gtg ctg cgg gcc caa gag tta gtg ctc cag ttg cat gca ctg	432
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu	
130 135 140	
cag ctg gac cgc cag gag ttc gtc tgt ctc aag ttc ctc atc ctc ttc	480
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe	
145 150 155 160	
agc ctc gat gtg aaa ttc ctg aac aac cac agc ctc gta aag gac gcc	528
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala	
165 170 175	
cag gaa aag gcc aac gct gcc ctg ttg gat tac acc ttg tgt cac tac	576
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Cys His Tyr	
180 185 190	
cca cac tgc ggg gac aaa ttc cag cag ttg cta ttg tcg ctg gtg gag	624
Pro His Cys Gly Asp Lys Phe Gln Gln Leu Leu Leu Ser Leu Val Glu	
195 200 205	
gtg cgg gcc ctg agc atg cag gcc aag gag tac ctg tac cac aag cat	672
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His	
210 215 220	
ttg ggc aac gag atg ccc cgc aac aac ctt ctc att gag atg ctg cag	720
Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln	
225 230 235 240	
gcc aag cag act tga	735
Ala Lys Gln Thr *	

<210> 17

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic variant

<400> 17

Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu
1 5 10 15
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln

[illegible]

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<210> 18
<211> 735
<212> DNA
<213> Artificial Sequence
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<220> .
<223> synthetic variant

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<221> CDS
<222> (1) ... (735)
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<400> 18																
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Ser	Gly	Gly	Pro	Asn	Val	Pro	Glu	Leu	Ile	Leu	Gln	Leu	Leu	Gln	Leu	
1				5					10					15		
gag	cca	gag	gag	gac	cag	gtg	cgc	gct	cgc	atc	gtg	ggc	tgt	ctg	cag	96
Glu	Pro	Glu	Glu	Asp	Gln	Val	Arg	Ala	Arg	Ile	Val	Gly	Cys	Leu	Gln	
			20					25					30			
gag	cca	gcc	aaa	agc	cgc	tct	gac	cag	cca	gcg	ccc	ttc	agc	ctc	ctc	144
Glu	Pro	Ala	Lys	Ser	Arg	Ser	Asp	Gln	Pro	Ala	Pro	Phe	Ser	Leu	Leu	

35	40	45	
tgc aga atg gcc gac cag acc ttt atc tcc att gtc gac tgg gca cga			192
Cys Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg			
50	55	60	
agg tgc atg gtc ttt aag gag ctg gag gtg gct gac cag atg aca ctg			240
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu			
65	70	75	80
ctg cag aac tgt tgg agc gag ctg ctg gtg ttg gac cac atc tac cgc			288
Leu Gln Asn Cys Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg			
	85	90	95
cag gtc cag tac ggc aag gaa gac agc atc ctg ctg gtt act gga cag			336
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln			
	100	105	110
gag gtg gag ctg agc aca gtg gct gtg cag gct ggc tcc ctg ctg cac			384
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His			
	115	120	125
agc ctg gtg ctg cgg gcc caa gag tta gtg ctc cag ttg cat gca ctg			432
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu			
	130	135	140
cag ctg gac cgc cag gag ttc gtc tgt ctc aag ttc ctc atc ctc ttc			480
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe			
145	150	155	160
agc ctc gat gtg aaa ttc ctg aac aac cac agc ctc gta aag gac gcc			528
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala			
	165	170	175
cag gaa aag gcc aac gct gcc ctg ttg gat tac acc ttg agc cac tac			576
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Ser His Tyr			
	180	185	190
cca cac tcc ggg gac aaa ttc cag cag ttg cta ttg tgc ctg gtg gag			624
Pro His Ser Gly Asp Lys Phe Gln Gln Leu Leu Leu Cys Leu Val Glu			
	195	200	205
gtg cgg gcc ctg agc atg cag gcc aag gag tac ctg tac cac aag cat			672
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His			
	210	215	220
ttg ggc aac gag atg ccc cgc aac aac ctt ctc att gag atg ctg cag			720
Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln			
225	230	235	240
gcc aag cag act tga			735
Ala Lys Gln Thr *			

<210> 19
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic variant

<400> 19
Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu
1 5 10 15
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln
20 25 30
Glu Pro Ala Lys Ser Arg Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu
35 40 45
Cys Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg
50 55 60
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu
65 70 75 80
Leu Gln Asn Cys Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg
85 90 95
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln
100 105 110
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His
115 120 125
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu
130 135 140
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe
145 150 155 160
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala
165 170 175
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Ser His Tyr
180 185 190
Pro His Ser Gly Asp Lys Phe Gln Gln Leu Leu Leu Cys Leu Val Glu
195 200 205
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His
210 215 220
Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln
225 230 235 240
Ala Lys Gln Thr

<210> 20
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic variant

<221> CDS

<222> (1)...(735)

<400> 20

tca gga ggg ccc aat gta cca gag ctc ata ttg cag ctg ctg caa cta	48
Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu	
1 5 10 15	
gag cca gag gag gac cag gtg cgc gct cgc atc gtg ggc tgt ctg cag	96
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln	
20 25 30	
gag cca gcc aaa agc cgc tct gac cag cca gcg ccc ttc agc ctc ctc	144
Glu Pro Ala Lys Ser Arg Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu	
35 40 45	
tgc aga atg gcc gac cag acc ttt atc tcc att gtc gac tgg gca cga	192
Cys Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg	
50 55 60	
agg tgc atg gtc ttt aag gag ctg gag gtg gct gac cag atg aca ctg	240
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu	
65 70 75 80	
ctg caa aac tct tgg agc gag ctg ctg gtg ttg gac cac atc tac cgc	288
Leu Gln Asn Ser Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg	
85 90 95	
cag gtc cag tac ggc aag gaa gac agc atc ctg ctg gtt act gga cag	336
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln	
100 105 110	
gag gtg gag ctg agc aca gtg gct gtg cag gct ggc tcc ctg ctg cac	384
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His	
115 120 125	
agc ctg gtg ctg cgg gcc caa gag tta gtg ctc cag ttg cat gca ctg	432
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu	
130 135 140	
cag ctg gac cgc cag gag ttc gtc tgt ctc aag ttc ctc atc ctc ttc	480
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe	
145 150 155 160	
agc ctc gat gtg aaa ttc ctg aac aac cac agc ctc gta aag gac gcc	528
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala	
165 170 175	
cag gaa aag gcc aac gct gcc ctg ttg gat tac acc ttg agc cac tac	576
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Ser His Tyr	
180 185 190	
cca cac tcc ggg gac aaa ttc cag cag ttg cta ttg tcg ctg gtg gag	624

Pro His Ser Gly Asp Lys Phe Gln Gln Leu Leu Leu Ser Leu Val Glu
195 200 205

gtg cgg gcc ctg agc atg cag gcc aag gag tac ctg tac cac aag cat 672
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His
210 215 220

ttg ggc aac gag atg ccc cgc aac aac ctt ctc att gag atg ctg cag 720
Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln
225 230 235 240

gcc aag cag act tga 735
Ala Lys Gln Thr *

<210> 21
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic variant

<400> 21
Ser Gly Gly Pro Asn Val Pro Glu Leu Ile Leu Gln Leu Leu Gln Leu
1 5 10 15
Glu Pro Glu Glu Asp Gln Val Arg Ala Arg Ile Val Gly Cys Leu Gln
20 25 30
Glu Pro Ala Lys Ser Arg Ser Asp Gln Pro Ala Pro Phe Ser Leu Leu
35 40 45
Cys Arg Met Ala Asp Gln Thr Phe Ile Ser Ile Val Asp Trp Ala Arg
50 55 60
Arg Cys Met Val Phe Lys Glu Leu Glu Val Ala Asp Gln Met Thr Leu
65 70 75 80
Leu Gln Asn Ser Trp Ser Glu Leu Leu Val Leu Asp His Ile Tyr Arg
85 90 95
Gln Val Gln Tyr Gly Lys Glu Asp Ser Ile Leu Leu Val Thr Gly Gln
100 105 110
Glu Val Glu Leu Ser Thr Val Ala Val Gln Ala Gly Ser Leu Leu His
115 120 125
Ser Leu Val Leu Arg Ala Gln Glu Leu Val Leu Gln Leu His Ala Leu
130 135 140
Gln Leu Asp Arg Gln Glu Phe Val Cys Leu Lys Phe Leu Ile Leu Phe
145 150 155 160
Ser Leu Asp Val Lys Phe Leu Asn Asn His Ser Leu Val Lys Asp Ala
165 170 175
Gln Glu Lys Ala Asn Ala Ala Leu Leu Asp Tyr Thr Leu Ser His Tyr
180 185 190
Pro His Ser Gly Asp Lys Phe Gln Gln Leu Leu Leu Ser Leu Val Glu
195 200 205
Val Arg Ala Leu Ser Met Gln Ala Lys Glu Tyr Leu Tyr His Lys His
210 215 220

Leu Gly Asn Glu Met Pro Arg Asn Asn Leu Leu Ile Glu Met Leu Gln
225 230 235 240
Ala Lys Gln Thr

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<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence
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<220>
<223> synthetic construct

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<221> VARIANT
<222> 6
<223> Xaa=Q/G
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<400> 22
Glu Asn Leu Tyr Phe Xaa Thr Cys Ser
1 5

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<210> 23
<211> 6
<212> PRT
<213> Artificial Sequence
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<220>
<223> synthetic construct

<400> 23
Leu Leu Ile Glu Met Leu
1 5

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<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence
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<220>
<223> synthetic construct

<400> 24
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

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<210> 25
<211> 9
<212> PRT
<213> Artificial Sequence
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<220>

<223> synthetic construct

<400> 25

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5

<210> 26

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 26

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

1 5 10

<210> 27

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 27

Asp Thr Tyr Arg Tyr Ile

1 5

<210> 28

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 28

tcggccattc gcgagaggag gctg

24

<210> 29

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 29
ctcgctccaa gagttttgca gcagtg 26

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 30
cacctccacc agcgacaata gcaac 25

<210> 31
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 31
tacaccttga gccactaccc acaactccggg gacaaattcc 40

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 32
ctatccagag ggatcctcag gagg 24

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 33
aggagtcttc tcgaggcagt ggca 24